Supplementary Text T6

Publicly available mapped positions of IMR90 [1] were downloaded from the Gene Expression Omnibus (GEO) [2]. Using the IMR90 data set, we have first generated a 10Kb contact map for the region 26-28Mb in chromosome 7. We have then computed the 1D contact profile (the row sums) of the latter contact map and segmented the 1Mb region (27-28Mb) surrounding the HOXA locus using our change point approach (described in the paper). The resulting change points were found in positions 27,230,000 and 27,520,000 (Figure T6.1), matching the boundaries of key genomic features and in agreement with the boundaries found by Dixon *et al.* [1].

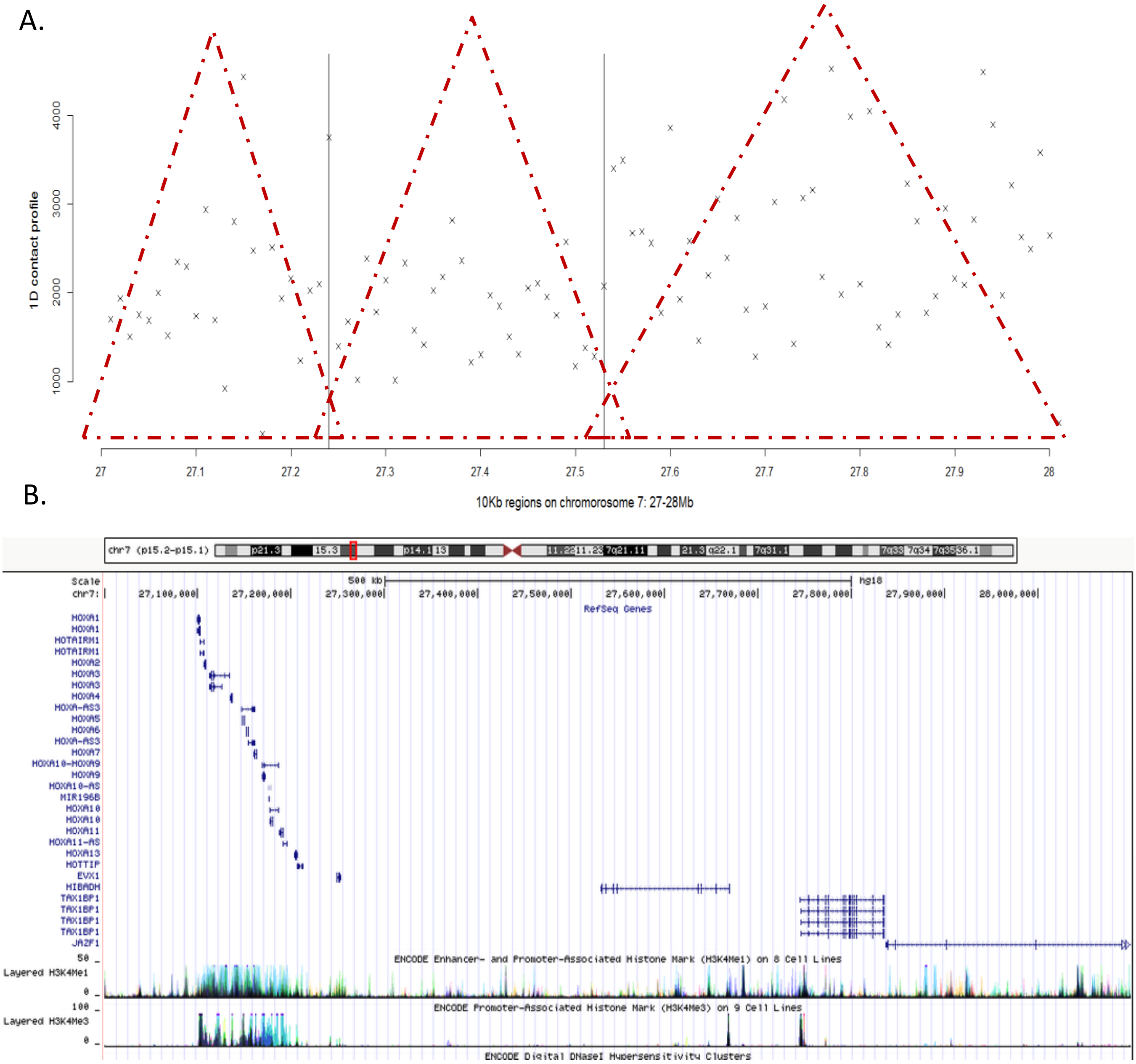

Figure T6.1. Change points identified in the contact profile of the 1Mb region (27-28Mb) surrounding the HOXA locus. A. Change points (the boundaries of domains) are marked with a black line and red triangles represent topological domains. The identified boundaries are also in agreement with the boundaries detected by Dixon *et al.* [1] B. A snapshot of the 1Mb (27-28Mb) region surrounding the HOXA locus, as available from the UCSC genome browser [3] (genome reference *hg18; http://genome-euro.ucsc.edu/cgi-bin/hgTracks?db=hg18&position=chr7%3A27000000-28000000*), showing that our detected change points mark boundaries consistent with key genomic features.

References

1. Dixon JR, Selvaraj S, Yue F, Kim A, Li Y, Shen Y, Hu M, Liu JS and Ren B: **Topological domains in mammalian genomes identified by analysis of chromatin interactions**. *Nature* 2012, **485**:376–80.
2. Edgar R, Domrachev M and Lash AE: **Gene Expression Omnibus: NCBI gene expression and hybridization array data repository**. *Nucl. Acids Res*. 2002, **30**:207-10.
3. Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM, Haussler D**. The human genome browser at UCSC**. *Genome Res*. 2002, **12**:996-1006.